

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.16 [Mar-25-2007]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x\_dropoff: 0 expect: 10.0000 wordsize: 11 Filter View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

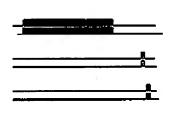
Show CDS translation Align:

13 18357 87

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**Sequence 1**: lcl|seq\_1 Length = 4867 (1 .. 4867)

Sequence 2: lcl|seq\_2 Length = 4936 (1 .. 4936)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

EXHIBIT Score = 3012 bits (1566), Expect = 0.0 Identities = 2570/3067 (83%), Gaps = 6/3067 (0%) Strand=Plus/Plus 357 TGGGCGAGGGCTGTCCTCAGAAGCTGGTGACTGCTAACTTGCTGCGCTTCCTCCTGCTGG Query TGGGCAATGGCTGCTCAGAAGCTGGCGACTGCTAACCTCCTCCGGTTCCTATTGCTGG 189 Sbjct TGCTCATCCCCTGCATCTGCGCCCTCATCGTGCTGCTGGCCATCCTGCTGTCCTTTGTGG 476 Query 417 308 TCCTGATTCCATGTATCTGTGCTCTCGTTCTCTTGCTGGTGATCCTGCTTTCCTATGTTG Sbjct 249 477 GAACATTAAAAAGGGTTTATTTCAAATCAAATGACAGTGAACCTTTGGTCACTGATGGGG 536 Query GAACATTACAAAAGGTCTATTTTAAATCAAATGGGAGTGAACCTTTGGTCACTGATGGTG Sbjct 309

.7% 0300

Query	537	AAGCTCGAGTGCCTGGTGTTATTCCTGTAAATACAGTTTATTATGAGAACACAGGGGCGC	596
Sbjct	369	AAATCCAAGGGTCCGATGTTATTCTTACAAATACAATTTATAACCAGAGCACTGTGGTGT	428
Query	597	CCTCTCTGCCCCCCAGCCAGTCCACTCCAGCCTGGACACCGAGAGCTCCTTCTCCAGAGG	656***
Sbjct	429		488
Query	657	ACCAGAGTCACAGGAACACAAGCACCTGCATGAACATCACTCAC	716
Sbjct	489	ACCAAAGTCACAGGAATACAAGTGCCTGTATGAACATCACCCACAGCCAGTGTCAGATGC	548
Query	717	TGCCCTACCACAGCACGTTGGCACCTCTCTTGCCAATTGTCAAAAACATGGACATGGAGA	776
Sbjct	549	TGCCTACCACGCCACGCTGACACCTCTCCTCTCAGTTGTCAGAAACATGGAAATGGAAA	
Query	777	AGTTCCTCAAGTTCTTCACGTACCTCCATCGCCTCAGTTGCTATCAACATATCCTGCTCT	836
Sbjct	609	AGTTCCTCAAGTTTTTCACATATCTCCATCGCCTCAGTTGCTATCAACATATCATGCTGT	668
Query	837	TCGGCTGTAGCCTCGCCTTCCCTGAGTGCGTTGTTGATGGCGATGACAGGCATGGTCTTC	896
Sbjct	669	TTGGCTGTACCCTCGCCTTCCCTGAGTGCATCATTGATGGCGATGACAGTCATGGACTCC	728
Onerl	897	TACCCTGTAGATCTTTCTGTGAGGCTGCAAAAGAAGGATGCGAATCTGTCCTGGGAATGG	95 <i>6</i>
Sbjct	729	TGCCCTGTAGGTCCTTCTGTGAGGCTCCAAAAGAAGGCTGTGAATCAGTCCTGGGGATGG	. 789
Query	957	TGAACTCCTCCTGGCCGGATTCCCTCAGATGCTCTCAGTTTAGGGACCACACTGAGACTA	1016
Sbjct	789	TGAATTACTCCTGGCCGGATTTCCTCAGATGCTCCCAGTTTAGAAACCAAACTGAAAG	846
Query	1017	ACAGCAGTGTCAGAAAGAGCTGCTTCTCACTGCAGCAGGAACATGGAAAGCAATCACTCT	1076
Sbjct	847	- cágcáatgtcágcágaatttgcttctcácctcágcágcágááaacggáááagcáattgctct	905
Query	1077	GTGGAGGGGGGGAGAGCTTCCTGTGTACCAGCGGGCTCTGCGTCCCCAAGAAGCTGCAGT	1136
Sbjct	906	GTGGAAGGGTGAGAACTTTCTGTGTGCCAGTGGAATCTGCATCCCCGGGAAACTGCAAT	965
Query	1137	GTAACGGCTATAATGACTGTGATGACTGGAGCGACGAGGCGCATTGCAACTGCAGCAAGG	1196
Sbjct	966	ĠŤÄÄTGGCTACAACGACTGTGACGACTGGAGTGACGAGGCTCATTGCAACTGCAGCGAGA	1025
Query	1197	ATCTGTTTCACTGTGGCACAGGCAAGTGCCTCCACTACAGCCTCTTGTGTGATGGGTACG	1256
Sbjct	1026	ATCTGTTTCACTGTCACACAGGCAAGTGCCTTAATTACAGCCTTGTGTGATGGATATG	1095
Query	1257	ATGACTGTGGGGACCCGAGTGACGAGCAAAACTGTGATTGTAATCTCACAAAAGAGCATC	1316
Sbjct	1086	ATGACTGTGGGGATTTGAGTGATGAGCAAAACTGTGATTGCAATCCCACAACAGAGCATC	1145
Query	1317	GCTGTGGAGATGGGCCTGCATTGCGGCTGAGTGGGTGTGCGATGGGGACCATGACTGTG	1376
Sbjct	1146	GCTGCGGGGACGGCGCTGCATCGCCATGGAGTGGGTGTGTGATGGTGACCACGACTGTG	1205
Query	1377	TGGACAAGTCTGATGAGGTCAACTGCTCTTGTCACAGCCAGGGCCTGGTGGAATGCACAA	1436
Sbjct	1206	TGGATAAGTCCGACGAGGTCAACTGCTCCTGTCACAGCCAGGGTCTGGTGGAATGCAGAA	1265

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Que	ry 1437	GTGGACAGTGCATCCCTAGCACCTTCCAGTGTGATGGGACGAAGACTGTAAGGATGGGA	1496
Sbj	ct 1266		1325
- 75 Que	ry 1497	GTGACGAGGAGAACTGCAGTGACAGTCAGACGCCATGTCCAGAAGGAGAACAGGGATGCT	1556
; · Sbj	ct 1326		1385
Que	ry 1557	TTGGCAGTTCCTGCGAATCCTGTGCTGGTAGCTCTCTGTGTGACTCAGACAGCAGCC	1616
. Sbj	ct 1386		1445
7ઇંટ Que	ry 1617	TGAGTAACTGCAGTCAATGTGAGCCCATCACTTTGGAACTCTGCATGAATTTGCTCTACA	1676
a.e.g. Sbj	ct 1446		1505
Que	ry 1677	ACCATACACATTATCCAAATTACCTTGGCCACAGAACTCAAAAGGAAGCGTCCATCAGCT	1736
Sbj	ct 1506		1565
Que	ry 1737	GGGAGTCATCCCTTTTCCCTGCCCTTGTACAAACCAACTGTTACAAATACCTCATGTTTT	1796
Sbj	ct 1566	GGGAGTCTTCTCTTTTCCCTGCACTTGTTCAAACCAACTGTTATAAATACCTCATGTTCT	1625
Que	ry 1797	TCGCTTGCACCATTTTGGTTCCAAAGTGTGATGTGAATACAGGACAACGCATCCCGCCTT	1856
Sbj	ct 1626	TTTCTTGCACCATTTTGGTACCAAAATGTGATGTGAATACAGGCGAGCGTATCCCTCCTT	1685
Que	гу 1857	GCAGACTCCTGTGTGAGCACTCCAAAGAGCGCTGTGAGTCTGTTCTGGGAATCGTTGGCC	1916
Sbj	ct 1686		1745
Que	ry 1917	TGCAGTGGCCTGAAGACACCGACTGCAATCAATTTCCAGAGGAAAGTTCAGACAATCAAA	1976
. Sbj	ct 1746		1805
Que	ry 1977	CTTGCCTCCTGCCCAATGAAGATGTGGAAGAATGCTCTCCGAGTCACTTCAAATGCCGCT	2036
\$bj	ct 1806	CCTGCCTGATGCCTGATGAATATGTGGAAGAATGCTCACCTAGTCATTTCAAGTGCCGCT	1865
Que	ry 2037	CGGGACGATGCGTTCTGGGCTCCAGGAGATGTGACGGCCAGGCTGACTGTGACGACGACA	2096
Sbj	st 1866		1925
Que	cy 2097	GTGACGAGGAGACTGTGGTTGTAAAGAGAGAGCTCTTTGGGAATGTCCATTTAATAAGC	2156
Sbj	t 1926	GTGATGAGGAAAACTGTGGTTGTAAAGAGAGAGATCTTTGGGAATGTCCATCCA	1985
Que	ry 2157	AATGTCTGAAGCATACATTAATCTGCGATGGGTTTCCAGATTGTCCAGACAGTATGGATG	2216
Sbj	t 1986		2045
Quei	ry 2217	AAAAAACTGCTCATTTTGCCAAGACAATGAGCTGGAATGTGCCCAACCATGAGTGTGTGC	2276
Sbjo	t 2046	AGAAAAACTGCTCATTTTGCCAAGATGATGAGCTGGAATGTGCAAACCATGCGTGTGTT	2105
Quei	ry 2277	CGCGTGACCTTTGGTGCGACGGATGGGTCCACTGCTCAGACAGTTCTGATGAATGGGGCT	2336
S <b>b</b> j0	t 2106	CACCTGACCTGTGGTGATGGTGAAGCCGACTGCTCAGACAGTTCAGATGAATGGGACT	2165

Query	2337	GTGTGACCCTCTCTAAAAATGGGAACTCCTCCTCATTGCTGACTGTTCACAAATCTGCAA	2396	
Sbjct	2166	GTGTGACCCTCTATAAATGTGAACTCCTCTTCCTTTCTGATGGTTCACAGAGCTGCCA	2225	
Query"	2397	AGGAACACCACGTGTGTGCTGACGGCTGGCGGGAGACGTTGAGTCAGCTGGCCTGCAAGC	2456 (100.3)	Etc. 1.
Sbjct	2226	CAGACACCATGTGTGTGCAGATGGCTGGCAGGAGATATTGAGTCAGCTGGCCTGCAAGC	2285 🗀 🚉	<b>2</b> -:
Query	2457	AGATGGGTTTAGGAGAACCGTCTGTGACCAAGCTGATCCCAGGACAGGAAGGCCAGC	2513	
Sbjct	2286		2345	1.
Onery	2514	AGTGGCTGAGGTTGTACCCCAACTGGGAGAATCTCAATGGGAGCACCTTGCAGGAGCTGC	2573	
<b>Sb</b> jat	2346		्र 2405 हम्बर नामक्ष्य <u>ः</u> - 2405 हम्बर नामक्ष्यः	
Query	2574	TGGTATACAGGCACTCCTGCCCAAGCAGAAGTGAGATTTCCCTTCTGTGCTCCAAGCAAG	2633 –	Jane
Sbjct	2406		2465	
Query	2634	ACTGTGGCCGCCCTGCTGCCCGAATGAACAAGAGGATCCTTGGGGGTCGGACTAGTC	2693	
Sbjat	2466	ACTGTGGGCGCCCTGCTGCCCGAATGAACAAAAGGATCCTTGGAGGTCGGACGAGTC	2525	
Query	2694	GTCCTGGGAGGTGGCCGTGGCAGTGCTCTCTGCAGAGTGAACCCAGTGGACATATCTGTG	2753	
Sbjct	2526		2585	
Query	2754	GCTGTGTCCTCATTGCCAAGAAGTGGGTCCTGACAGTTGCCCATTGCTTTGAAGGGAGAG	2813	
Sbjct	2586	GCTGTGTCCTCATTGCCAAGAAGTGGGTTCTGACAGTTGCCCACTGCTTCGAGGGGAGAG	2645	••
Query	2814	AAGACGCTGATGTTTGGAAAGTGGTATTTGGCATAAACAACCTGGACCATCCAT	2873	
Sbjct	2646	AGAATGCTGCAGTTTGGAAAGTGGTGCTTGGCATCAACAATCTAGACCATCCAT	2705	-
Query	2874	TCATGCAGACCCGCTTTGTGAAGACCATCCTGCTACATCCCCGTTACAGTCGAGCAGTGG	2933	
Sbjct	2706	TCATGCAGACACGCTTTGTGAAGACCATCATCCTGCATCCCCGCTACAGTCGAGCAGTGG	2765	
Query	2934	TAGACTATGATATCAGCGTGGTGGAGCTGAGCGATGATATCAATGAGACAAGCTACGTCA	2993	
Sbjct	2766		2825	
Query	2994	GACCTGTCTGCCTACCCAGTCCGGAGGAGTATCTAGAACCAGATACGTACTGCTACATCA	3053	
Sbjct	2826	GGCCTGTCTGCCTACCCGGAGCAGTGGCTAGAGCCTGACACGTACTGCTATATCA	2885	
Query	3054	CAGGCTGGGGCCACATGGGCAATAAAATGCCCTTTAAGCTGCAGGAGGGAG	3113	
Sbjct	2886	CAGGCTGGGGCCACATGGGCAATAAAATGCCATTTAAGCTGCAAGAGGGAGAGGTCCGCA	2945	
Query	3114	TTATCCCTCTGGAGCAGTGCCAGTCCTATTTTGACATGAAGACCATCACCAATCGGATGA	3173	
Sbjct	2946	TTATTTCTCTGGAACATTGTCAGTCCTACTTTGACATGAAGACCATCACCACTCGGATGA	3005	
Query	3174	TCTGTGCTGGCTATGAGTCTGGCACCGTGGACTCCTGCATGGGAGACAGCGGTGGGCCTC	3233	
Sbjct	3006	TATGTGCTGGCTATGAGTCTGGCACAGTTGATTCATGCATG	3065	

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Page 5 of 5

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Blast Result
```

Query	3234	TGGTTTGTGAACGACCCGGAGGACAGTGGACATTATTTGGTTTAACTTCATGGGGCTCCG	3293 3
Sbjct	3066		3125
Query	3294	TCTGCTTTTCCAAAGTTCTGGGACCTGGAGTGTACAGCAATGTGTCTTACTTTGTGGGCT	3353 1993 1991
Sbjct	3126	TCTGCTTTTCCAAAGTCCTGGGGCCTGGCGTTTATAGTAATGTGTCATATTTCGTCGAAT	3185
Query	3354	GGATTGAAAGACAAATATATATCCAGACCTTTCTCCAAAAGAAATCCCAAGGATAATCAG	3413
Sbjct	3186	GGATTAAAAGACAGATTTACATCCAGACCTTTCTCCTAAACTAATTATAAGGATGATCAG	3245
Query	3414	AGACTTT 3420 572.71 5 20 20 20 20 20 20 20 20 20 20 20 20 20	***
Sbjct	3246	AGACTTT 3252	meter an an deference of
		·	•

74/24/201

Score = 100 bits (52), Expect = 5e-17 Identities = 94/115 (81%), Gaps = 0/115 (0%) Strand=Plus/Plus

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Query 4411 AAATTTTAAGGATGCTTTTAAGCACTGGGCCACTTTATGGGAATCAATTCCCAAAGCAAT 4470 ...
         Sbjct 4412 AAATTTTAGAAATGATTTTTAGCTCTAGGCCACTTTACGCAACTCAATTTCTGAAGCAAT 4471
Query 4471 TAGTGGTTACAAGTATTTTTTCCCACTAAAAAGTTTCAAAACACAAACCTTCATA 4525
         TAGTGGTAAAAAGTATTTTTCCCCACTAAAAAACTTTAAAACACAAATCTTCATA 4526
Sbjct 4472
```

141797

Score = 62.2 bits (32), Expect = 2e-05 Identities = 77/97 (79%), Gaps = 1/97 (1%) Strand=Plus/Plus

CPU time:

TTTTGAACAAGTAGGATGCACTGTTAAACTTCACCAGCAACCAA-ACTGCCTCAGTATTG 4629 Query 4571 TTTTAAACAACTAGGATTCCCTACTAACCTCCACCAGCAACCTGGACTGCCTCAGCATTC 4622 Sbjct 4563 Query 4630 CTTACAGGGACTACCTGCAATTTTATATGTGTATTTT 4666 Sbict 4623 CAAATAGATACTACCTGCAATTTTATACATGTATTTT

0.03 user secs. 0.01 sys. secs

0.04 total secs.

Blast Result

Page 1 of z



## **Blast 2 Sequences results**



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Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.16 [Mar-25-2007]

Matrix BLOSUM62 gap open: 11 gap extension: 1 expect: 10.0000 wordsize: 3 x dropoff: 0 Filter W. View option Standard Masking character option X for protein, n for nucleotide Masking color option Black Show CDS translation | Align in hower.

Sequence 1: lcl|seq\_1 Length = 1113 (1 ... 1113)

Sequence 2: lcl|seq\_2 Length = 1042 (1 ... 1042)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 1658 bits (4293), Expect = 0.0, Method: Composition-based stats. Identities = 849/1023 (82%), Positives = 921/1023 (90%), Gaps = 2/1023 (0%)

Query	86	PAPDVLRADRSVGEGCPQKLVTANLLRFLLLVLIPCICALIVLLAILLSFVGTLKRVYFK P P + D ++G GC OKL TANLLRFLLLVLIPCICAL++LL ILLS+VGTL++VYFK	145
Sbjct	19	PKPVLRADDNNMGNGCSQKLATANLLRFLLLVLIPCICALVLLLVILLSYVGTLQKVYFK	78
Query	146	SNDSEPLVTDGEARVPGVIPVNTVYYENTGAPSLPPSQSTPAWTPRAPSPEDQSHRNTST SN SEPLVTDGE + VI NT+Y ++T + P Q PAWT A P DQSHRNTS	205
Sbjct	79	SNGSEPLVTDGEIQGSDVILTNTIYNQSTVVSTAHPDQHVPAWTTDASLPGDQSHRNTSA	138
Query	206	CMNITHSQCQILPYHSTLAPLLPIVKNMDMEKFLKFFTYLHRLSCYQHILLFGCSLAFPE CMNITHSOCO+LPYH+TL PLL +V+NM+MEKFLKFFTYLHRLSCYOHI+LFGC+LAFPE	265
Sbjct	139	CMNITHSQCQMLPYHATLTPLLSVVRNMEMEKFLKFFTYLHRLSCYQHIMLFGCTLAFPE	198
Query	266	CVVDGDDRHGLLPCRSFCEAAKEGCESVLGMVNSSWPDSLRCSQFRDHTETNSSVRKSCF	325
Sbjct	199	C++DGDD HGLLPCRSFCEAAKEGCESVLGMVN SWPD LRCSQFR+ TE+ S+V + CF CIIDGDDSHGLLPCRSFCEAAKEGCESVLGMVNYSWPDFLRCSQFRNQTES-SNVSRICF	257

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Query	326	SLQQEHGKQSLCGGGBSFLCTSGLCVPKKLQCNGYNDCDDWSDBAHCNCSKDLFHCGTGK 385 S QQE+GKQ LCG GE+FLC SG+C+P KLQCNGYNDCDDWSDBAHCNCS++LFHC TGK	
Sbjct	258	SPQQENGKQLLCGRGENFLCASGICIPGKLQCNGYNDCDDWSDEAHCNCSENLFHCHTGK -317	
Query	386	CLHYSLLCDGYDDCGDPSDEQNCDCNLTKEHRCGDGRCIAAEWVCDGDHDCVDKSDEVNC 445 CL+YSL+CDGYDDCGD SDEQNCDCN T EHRCGDGRCIA EWVCDGDHDCVDKSDEVNC	
Sbjct	318	CLNYSLVCDGYDDCGDLSDEQNCDCNPTTEHRCGDGRCIAMEWVCDGDHDCVDKSDEVNC 377	
Query	446	SCHSQGLVECTSGQCIPSTFQCDGDEDCKDGSDEENCSDSQTPCPEGEQGCFGSSCVESC 505 SCHSQGLVEC +GQCIPSTFQCDGDEDCKDGSDEENCS QT C EG+Q C + C++SC:	
Sbjct	378	SCHSQGLVECRNGQCIPSTFQCDGDEDCKDGSDEENCSVIQTSCQEGDQRCLYNPCLDSC 437	
Query	506	AGSSLCDSDSSLSNCSQCEPITLELCMNLLYNHTHYPNYLGHRTQKEASISWESSLPPAL: 565	
Sbjct	438	GSSLCD: ++SL+NCSQCEPITLELCMNL YN T YPNY GHRTQKEASISWESSLFPAL: 497 GGSSLCDPNNSLNNCSQCEPITLELCMNLPYNSTSYPNYFGHRTQKEASISWESSLFPAL: 497	
Query	566	VQTNCYKYLMFFACTILVPKCDVNTGQRIPPCRLLCEHSKERCESVLGIVGLQWPEDTDC 625 VQTNCYKYLMFF+CTILVPKCDVNTG+RIPPCR LCEHSKERCESVLGIVGLQWPEDTDC	
Sbjct	498	VQTNCYKYLMFFSCTILVPKCDVNTGERIPPCRALCEHSKERCESVLGIVGLQWPEDTDC 557	
Query	626	NQFPEESSDNQTCLLPNEDVEECSPSHFKCRSGRCVLGSRRCDGQADCDDDSDEENCGCK 685 +QFPEE+SDNQTCL+P+E VEECSPSHFKCRSG+CVL SRRCDGQADCDDDSDEENCGCK	
Sbjct	558	SQFPEENSDNQTCLMPDEYVEECSPSHFKCRSGQCVLASRRCDGQADCDDDSDEENCGCK 617	
Query	686	ERALWECPFNKQCLKHTLICDGFPDCPDSMDEKNCSFCQDNELECANHECVPRDLWCDGW 745 ER LWECP NKQCLKHT+ICDGFPDCPD MDEKNCSFCOD+ELECANH CV RDLWCDG	
Sbjct	618	ERDLWECPSNKQCLKHTVICDGFPDCPDYMDEKNCSFCQDDELECANHACVSRDLWCDGE 677	
Query	746	VDCSDSSDEWGCVTLSKNGNSSSLLTVHKSAKEHHVCADGWRETLSQLACKQMGLGEPSV 805 DCSDSSDEW CVTLS N NSSS L VH++A EHHVCADGW+E LSQLACKQMGLGEPSV	
Sbjct	678	ADCSDSSDEWDCVTLSINVNSSSFLMVHRAATEHHVCADGWQEILSQLACKQMGLGEPSV 737	
Query	806	TKLIPGQEGQ-QWLRLYPNWENLNGSTLQELLVYRHSCPSRSEISLLCSKQDCGRRPAAR 864 TKLI QE + +WL L+ NWE+LNG+TL ELLV SC SRS+ISLLC+KQDCGRRPAAR	
Sbjct	738	TKLIQEQEKEPRWLTLHSNWESLNGTTLHELLVNGQSCESRSKISLLCTKQDCGRRPAAR 797	
Query	865	MNKRILGGRTSRPGRWPWQCSLQSEPSGHICGCVLIAKKWVLTVAHCFEGREDADVWKVV 924 MNKRILGGRTSRPGRWPWQCSLQSEPSGHICGCVLIAKKWVLTVAHCFEGRE+A VWKVV	
Sbjat	798	MNKRILGGRTSRPGRWPWQCSLQSBPSGHICGCVLIAKKWVLTVAHCFEGRENAAVWKVV 857	
Query	925	FGINNLDHPSGFMQTRFVKTILLHPRYSRAVVDYDISVVELSDDINETSYVRPVCLPSPE 984 GINNLDHPS FMQTRFVKTI+LHPRYSRAVVDYDIS+VELS+DI+ET YVRPVCLP+PE	
Sbjct	858	LGINNLDHPSVFMQTRFVKTIILHPRYSRAVVDYDISIVELSEDISETGYVRPVCLPNPE 917	
Query	985	EYLEPDTYCYITGWGHMGNKMPFKLQEGEVRIIPLBQCQSYFDMKTITNRMICAGYESGT 1044 ++LEPDTYCYITGWGHMGNKMPFKLQEGEVRII LE CQSYFDMKTIT RMICAGYESGT	ı
Sbjct	918	QWLEPDTYCYITGWGHMGNKMPFKLQEGEVRIISLEHCQSYFDMKTITTRMICAGYESGT 977	
Query	1045	VDSCMGDSGGPLVCERPGGQWTLFGLTSWGSVCFSKVLGPGVYSNVSYFVGWIERQIYIQ 1104 VDSCMGDSGGPLVCE+PGG+WTLFGLTSWGSVCFSKVLGPGVYSNVSYFV WI+RQIYIQ	:
Sbjct	978	VDSCMGDSGGPLVCEKPGGRWTLFGLTSWGSVCFSKVLGPGVYSNVSYFVEWIKRQIYIQ 1037	1
Query	1105	TFL 1107 TFL	
Sbjct	1038	TFL 1040	

CPU time: 0.03 user secs. 0.01 sys. secs

0.04 total secs.